



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/265,120
Source: IFWO
Date Processed by STIC: 9/1/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE~~ CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10765,120

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 J Misaligned Amino The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:36

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

1 <110> APPLICANT: Benner, Steven Albert
W--> 2 <120> TITLE OF INVENTION: Evolution-Based Functional Genomics
W--> 3 <140> CURRENT APPLICATION NUMBER: 10/765,120
W--> 0 <130> FILE REFERENCE:
4 <141> CURRENT FILING DATE: 2004-01-28
W--> 5 <160> NUMBER OF SEQ ID: 38
6 <170> SOFTWARE: MacIntosh OS 10.3 Microsoft Word v. 2003

ERRORED SEQUENCES

938 <210> SEQ ID NO: 14
939 <211> LENGTH: 478
940 <212> TYPE: PRT
941 <213> ORGANISM: Oryctolagus cuniculus
W--> 942 <400> SEQUENCE: 14
943 Met Leu Leu Glu Val Leu Asn Pro Arg His Tyr Asn Val Thr Ser
E--> 944 ~~005~~ 5 ~~010~~ 10 ~~015~~ 15
945 Met Val Ser Glu Val Val Pro Ile Ala Ser Ile Ala Ile Leu Leu
946 ~~020~~ 20 ~~025~~ 25 ~~030~~ 30
947 Leu Thr Gly Phe Leu Leu Leu Val Trp Asn Tyr Glu Asp Thr Ser
948 ~~035~~ 35 ~~040~~ 40 ~~045~~ 45
949 Ser Ile Pro Gly Pro Ser Tyr Phe Leu Gly Ile Gly Pro Leu Ile
950 ~~050~~ 50 ~~055~~ 55 ~~060~~ 60
951 Ser His Cys Arg Phe Leu Trp Met Gly Ile Gly Ser Ala Cys Asn
952 ~~065~~ 65 ~~070~~ 70 ~~075~~ 75
953 Tyr Tyr Asn Lys Met Tyr Gly Glu Phe Met Arg Val Trp Val Cys
954 ~~080~~ 80 ~~085~~ 85 ~~090~~ 90
955 Gly Glu Glu Thr Leu Ile Ile Ser Lys Ser Ser Ser Met Phe His
956 ~~095~~ 95 100 105
957 Val Met Lys His Ser His Tyr Ile Ser Arg Phe Gly Ser Lys Leu
958 110 115 120
959 Gly Leu Gln Phe Ile Gly Met His Glu Lys Gly Ile Ile Phe Asn
960 125 130 135
961 Asn Asn Pro Ala Leu Trp Lys Ala Val Arg Pro Phe Phe Thr Lys
962 140 145 150
963 Ala Leu Ser Gly Pro Gly Leu Val Arg Met Val Thr Ile Cys Ala
964 155 160 165
965 Asp Ser Ile Thr Lys His Leu Asp Arg Leu Glu Glu Val Cys Asn
966 170 175 180
967 Asp Leu Gly Tyr Val Asp Val Leu Thr Leu Met Arg Arg Ile Met
968 185 190 195
969 Leu Asp Thr Ser Asn Met Leu Phe Leu Gly Ile Pro Leu Asp Glu

pp 1-7
Does Not Comply
Corrected Diskette Needed

← misaligned
amino acid
numbers
(see item 3
on error
summary
sheet)

Please delete
0's (zeros)
before two-digit
amino acid numbers.

(see sample
Sequence Listing
attached in back,
for example)

also, see 1-822 of
Sequence Rules

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:36

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

```

970          200          205          210
971 Ser Ala Ile Val Val Asn Ile Gln Gly Tyr Phe Asp Ala Trp Gln
972          215          220          225
973 Ala Leu Leu Leu Lys Pro Asp Ile Phe Phe Lys Ile Ser Trp Leu
974          230          235          240
975 Cys Arg Lys Tyr Glu Lys Ser Val Lys Asp Leu Lys Asp Ala Met
976          245          250          255
977 Glu Ile Leu Ile Ala Glu Lys Arg His Arg Ile Ser Thr Ala Glu
978          260          265          270
979 Lys Leu Glu Asp Ser Ile Asp Phe Ala Thr Glu Leu Ile Phe Ala
980          275          280          285
981 Glu Lys Arg Gly Glu Leu Thr Arg Glu Asn Val Asn Gln Cys Ile
982          290          295          300
983 Leu Glu Met Leu Ile Ala Ala Pro Asp Thr Met Ser Val Ser Val
984          305          310          315
985 Phe Phe Met Leu Phe Leu Ile Ala Lys His Pro Gln Val Glu Glu
986          320          325          330
987 Ala Ile Ile Arg Glu Ile Gln Thr Val Val Gly Glu Arg Asp Ile
988          335          340          345
989 Arg Ile Asp Asp Met Gln Lys Leu Lys Val Val Glu Asn Phe Ile
990          350          355          360
991 Asn Glu Ser Met Arg Tyr Gln Pro Val Val Asp Leu Val Met Arg
992          365          370          375
993 Lys Ala Leu Glu Asp Asp Val Ile Asp Gly Tyr Pro Val Lys Lys
994          380          385          390
995 Gly Thr Asn Ile Ile Leu Asn Leu Gly Arg Met His Arg Leu Glu
996          395          400          405
997 Phe Phe Pro Lys Pro Asn Glu Phe Thr Leu Glu Asn Phe Ala Lys
998          410          415          420
999 Asn Val Pro Tyr Arg Tyr Phe Gln Pro Phe Gly Phe Gly Pro Arg
1000          425          430          435
1001 Gly Cys Ala Gly Lys Tyr Ile Ala Met Val Met Met Lys Val Val
1002          440          445          450
1003 Leu Val Thr Leu Leu Arg Arg Phe His Val Gln Thr Leu Gln Gly
1004          455          460          465
1005 Arg Cys Val Glu Lys Met Gln Lys Lys Asn Asp Leu Ser Leu His
1006          470          475          480
1007 Pro Asp Glu Thr Arg Asp

```

E--> 1008

485

1151 <210> SEQ ID NO: 17

1152 <211> LENGTH: 486

1153 <212> TYPE: PRT

1154 <213> ORGANISM: Poephila guttata

W--> 1155 <400> SEQUENCE: 17

1156 Met Phe Leu Glu Met Leu Asn Pro Met His Tyr Asn Val Thr Ile

1157 ~~005~~ ~~010~~ ~~015~~

1158 Met Val Pro Glu Thr Val Pro Val Ser Ala Met Pro Leu Leu Leu

1159 ~~020~~ ~~025~~ ~~030~~

1160 Ile Met Gly Leu Leu Leu Ile Arg Asn Cys Glu Ser Ser Ser

see p.3, too

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:36

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|--------------------|-----|--------------------|-----|-----|-----|-----|-----|-----|--------------------|-----|-----|
| 1161 | | 035 | | 040 | | 045 | | | | | | | | | |
| 1162 | Ser | Ile | Pro | Gly | Pro | Gly | Tyr | Cys | Leu | Gly | Ile | Gly | Pro | Leu | Ile |
| 1163 | | | | 050 | | 055 | | | | | | | | 060 | |
| 1164 | Ser | His | Gly | Arg | Phe | Leu | Trp | Met | Gly | Ile | Gly | Ser | Ala | Cys | Asn |
| 1165 | | | | 065 | | 070 | | | | | | | | 075 | |
| 1166 | Tyr | Tyr | Asn | Lys | Met | Tyr | Gly | Glu | Phe | Met | Arg | Val | Trp | Ile | Ser |
| 1167 | | | | 080 | | 085 | | | | | | | | 090 | |
| 1168 | Gly | Glu | Glu | Thr | Leu | Ile | Ile | Ser | Lys | Ser | Ser | Ser | Met | Val | His |
| 1169 | | | | 095 | | 100 | | | | | | | | 105 | |
| 1170 | Val | Met | Lys | His | Ser | Asn | Tyr | Ile | Ser | Arg | Phe | Gly | Ser | Lys | Arg |
| 1171 | | | | 110 | | 115 | | | | | | | | 120 | |
| 1172 | Gly | Leu | Gln | Cys | Ile | Gly | Met | His | Glu | Asn | Gly | Ile | Ile | Phe | Asn |
| 1173 | | | | 125 | | 130 | | | | | | | | 135 | |
| 1174 | Asn | Asn | Pro | Ser | Leu | Trp | Arg | Thr | Val | Arg | Pro | Phe | Phe | Met | Lys |
| 1175 | | | | 140 | | 145 | | | | | | | | 150 | |
| 1176 | Ala | Leu | Thr | Gly | Pro | Gly | Leu | Ile | Arg | Met | Val | Glu | Val | Cys | Val |
| 1177 | | | | 155 | | 160 | | | | | | | | 165 | |
| 1178 | Glu | Ser | Ile | Lys | Gln | His | Leu | Asp | Arg | Leu | Gly | Asp | Val | Thr | Asp |
| 1179 | | | | 170 | | 175 | | | | | | | | 180 | |
| 1180 | Asn | Ser | Gly | Tyr | Val | Asp | Val | Val | Thr | Leu | Met | Arg | His | Ile | Met |
| 1181 | | | | 185 | | 190 | | | | | | | | 195 | |
| 1182 | Leu | Asp | Thr | Ser | Asn | Thr | Leu | Phe | Leu | Gly | Ile | Pro | Leu | Asp | Glu |
| E--> 1183 | | | | 200 200 | | 205 205 | | | | | | | 210 210 | | |
| 1184 | Ser | Ser | Ile | Val | Lys | Lys | Ile | Gln | Gly | Tyr | Phe | Asn | Ala | Trp | Gln |
| E--> 1185 | | | | 215 | | 220 | | | | | | | | 225 | |
| 1186 | Ala | Leu | Leu | Ile | Lys | Pro | Asn | Ile | Phe | Phe | Lys | Ile | Ser | Trp | Leu |
| E--> 1187 | | | | 230 | | 235 | | | | | | | | 240 | |
| 1188 | Tyr | Arg | Lys | Tyr | Glu | Arg | Ser | Val | Lys | Asp | Leu | Lys | Asp | Glu | Ile |
| E--> 1189 | | | | 245 | | 250 | | | | | | | | 255 | |
| 1190 | Glu | Ile | Leu | Val | Glu | Lys | Lys | Arg | Gln | Lys | Val | Ser | Ser | Ala | Glu |
| E--> 1191 | | | | 260 | | 265 | | | | | | | | 270 | |
| 1192 | Lys | Leu | Glu | Asp | Cys | Met | Asp | Phe | Ala | Thr | Asp | Leu | Ile | Phe | Ala |
| E--> 1193 | | | | 275 | | 280 | | | | | | | | 285 | |
| 1194 | Glu | Arg | Arg | Gly | Asp | Leu | Thr | Lys | Glu | Asn | Val | Asn | Gln | Cys | Ile |
| E--> 1195 | | | | 290 | | 295 | | | | | | | | 300 | |
| 1196 | Leu | Glu | Met | Leu | Ile | Ala | Ala | Pro | Asp | Thr | Met | Ser | Val | Thr | Leu |
| E--> 1197 | | | | 305 | | 310 | | | | | | | | 315 | |
| 1198 | Tyr | Val | Met | Leu | Leu | Leu | Ile | Ala | Glu | Tyr | Pro | Glu | Val | Glu | Thr |
| E--> 1199 | | | | 320 | | 325 | | | | | | | | 330 | |
| 1200 | Ala | Ile | Leu | Lys | Glu | Ile | His | Thr | Val | Val | Gly | Asp | Arg | Asp | Ile |
| E--> 1201 | | | | 335 | | 340 | | | | | | | | 345 | |
| 1202 | Arg | Ile | Gly | Asp | Val | Gln | Asn | Leu | Lys | Val | Val | Glu | Asn | Phe | Ile |
| E--> 1203 | | | | 350 | | 355 | | | | | | | | 360 | |
| 1204 | Asn | Glu | Ser | Leu | Arg | Tyr | Gln | Pro | Val | Val | Asp | Leu | Val | Met | Arg |
| E--> 1205 | | | | 365 | | 370 | | | | | | | | 375 | |
| 1206 | Arg | Ala | Leu | Glu | Asp | Asp | Val | Ile | Asp | Gly | Tyr | Pro | Val | Lys | Lys |
| E--> 1207 | | | | 380 | | 385 | | | | | | | | 390 | |
| 1208 | Gly | Thr | Asn | Ile | Ile | Leu | Asn | Ile | Gly | Arg | Met | His | Arg | Leu | Glu |
| E--> 1209 | | | | 395 | | 400 | | | | | | | | 405 | |

← misaligned
amino acid
numbers

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:36

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

1210 Tyr Phe Pro Lys Pro Asn Glu Phe Thr Leu Glu Asn Phe Glu Lys
 E--> 1211 410 415 420
 1212 Asn Val Pro Tyr Arg Tyr Phe Gln Pro Phe Gly Phe Gly Pro Arg
 E--> 1213 425 430 435
 1214 Ser Cys Ala Gly Lys Tyr Ile Ala Met Val Met Met Lys Val Val
 E--> 1215 440 445 450
 1216 Leu Val Thr Leu Leu Lys Arg Phe His Val Lys Thr Leu Gln Lys
 E--> 1217 455 460 465
 1218 Arg Cys Ile Glu Asn Met Pro Lys Asn Asn Asp Leu Ser Leu His
 E--> 1219 470 475 480
 1220 Leu Asp Glu Asp Ser Pro
 E--> 1221 485

1445 <210> SEQ ID NO: 35

1446 <211> LENGTH: 83

1447 <212> TYPE: DNA

1448 <213> ORGANISM: Sus scrofa

IMPORTANT: use lower-case letters
for nucleotides

W--> 1449 <400> SEQUENCE: 35

C--> 1450 caatcattac acgtgccgat ttggcagcaa acctggggttg gaatgcattg gcatgcatga 60

E--> 1451 aaaaggcatca tgtttaacaa taa

1453 <210> SEQ ID NO: 36

1454 <211> LENGTH: 84

1455 <212> TYPE: DNA

1456 <213> ORGANISM: Sus scrofa

W--> 1457 <400> SEQUENCE: 36

C--> 1458 tagtcactac acatcccgat ttggcagcaa acctggggttg cagttcattg gcatgcatga 60

E--> 1459 gaaaggcatt atattcaaca ataa

1461 <210> SEQ ID NO: 37

1462 <211> LENGTH: 84

1463 <212> TYPE: DNA

1464 <213> ORGANISM: Sus scrofa

W--> 1465 <400> SEQUENCE: 37

C--> 1466 cagtcactac acatcccgat tcggcagcaa acctggggttg gagtgcattg gcatgtatga 60

E--> 1467 gaagggcatc atatttaata atga

E--> 1469 <210> SEQ ID NO: 37 38 ← change to

1470 <211> LENGTH: 84

1471 <212> TYPE: DNA

1472 <213> ORGANISM: White lipped peccary

W--> 1473 <400> SEQUENCE: 37 38 ← change to

C--> 1474 cagtcactac acatcccgat tcggcagcaa acctggggttg cagttcattg gaatgcatga 60

E--> 1475 gaaaggcatc atatttaaca acaa

84 ← insert
cumulative
base total
at right
margin
of each
line

84
↑
insert

84 ← insert

84 ← insert

10/765,120 5

<210> 26

<211> 50

<212> PRT

<213> Ancestral sequence

<400> 26

Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp
005 010 015
Leu Leu His Leu Leu Ala Ser Ser Lys Ser Cys Pro Leu Pro Gln
020 025 030
Ala Arg Gly Leu Glu Thr Leu Glu Ser Leu Gly Gly Val Leu Glu
035 040 045
Ala Ser Leu Tyr Ser
050

invalid <213> response. see item 10 on

Even summary

sheet.

6

Please
consult

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001

<141> 1998-12-31

<150> US 08/999,999

<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1

<211> 389

<212> DNA

<213> Paramecium sp.

<220>

<221> CDS

<222> (279)...(389)

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.

<303> Journal of Genes

<304> 1

<305> 4

<306> 1-7

<307> 1988-06-31

<308> 123456

<309> 1988-06-31

| | | | | | | | |
|------------|------------|------------|------------|------------|------------|--|-----|
| <400> | 1 | | | | | | |
| agctgtagtc | attcctgtgt | cctcttctct | ctgggcttct | cacctgcta | atcagatctc | | 60 |
| agggagagtg | tcttgacct | cctctgcctt | tgcagcttca | caggcaggca | ggcaggcagc | | 120 |
| tgatgtggca | attgctggca | gtgccacagg | cttttcagcc | aggcttaggg | tgggttccgc | | 180 |
| cgcggcgcg | cggccctct | cgcgctctc | tcgcgcctct | ctctcgctct | cctctcgctc | | 240 |

7

```

ggacctgatt  aggtgagcag  gaggaggggg  cagtttagc      atg  gtt  tca  atg  ttc  agc  296
Met  Val  Ser  Met  Phe  Ser
1

ttg  tct  ttc  aaa  tgg  cct  gga  ttt  tgt  ttg  ttt  gtt  tgt  ttg  ttc  caa  344
Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu  Phe  Val  Cys  Leu  Phe  Gln
10 15 20

tgt  ccc  aaa  gtc  ctc  ccc  tgt  cac  tca  tca  ctg  cag  ccg  aat  ctt  389
Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser  Leu  Gln  Pro  Asn  Leu
25 30 35

<210>      2
<211>      37
<212>      PRT
<213>      Paramecium sp.

<400>      2
Met  Val  Ser  Met  Phe  Ser  Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu
1      5 10

Phe  Val  Cys  Leu  Phe  Gln  Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser
20 25 30

Leu  Gln  Pro  Asn  Leu
35

<210>      3
<211>      11
<212>      PRT
<213>      Artificial Sequence

<220>
<223>      Designed peptide based on size and polarity to act as a
linker between the alpha and beta chains of Protein XYZ.

<400>      3
Met  Val  Asn  Leu  Glu  Pro  Met  His  Thr  Glu  Ile
1      5 10

<210>      4
<400>      4
000

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[Annex VIII follows]

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:37

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

L:2 M:283 W: Missing Blank Line separator, <120> field identifier
L:3 M:283 W: Missing Blank Line separator, <140> field identifier
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:5 M:283 W: Missing Blank Line separator, <160> field identifier
L:12 M:283 W: Missing Blank Line separator, <400> field identifier
L:84 M:283 W: Missing Blank Line separator, <400> field identifier
L:156 M:283 W: Missing Blank Line separator, <400> field identifier
L:228 M:283 W: Missing Blank Line separator, <400> field identifier
L:300 M:283 W: Missing Blank Line separator, <400> field identifier
L:371 M:283 W: Missing Blank Line separator, <400> field identifier
L:443 M:283 W: Missing Blank Line separator, <400> field identifier
L:515 M:283 W: Missing Blank Line separator, <400> field identifier
L:585 M:283 W: Missing Blank Line separator, <400> field identifier
L:656 M:283 W: Missing Blank Line separator, <400> field identifier
L:728 M:283 W: Missing Blank Line separator, <400> field identifier
L:800 M:283 W: Missing Blank Line separator, <400> field identifier
L:872 M:283 W: Missing Blank Line separator, <400> field identifier
L:942 M:283 W: Missing Blank Line separator, <400> field identifier
L:944 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:1008 M:252 E: No. of Seq. differs, <211> LENGTH:Input:478 Found:486 SEQ:14
L:1014 M:283 W: Missing Blank Line separator, <400> field identifier
L:1086 M:283 W: Missing Blank Line separator, <400> field identifier
L:1155 M:283 W: Missing Blank Line separator, <400> field identifier
L:1183 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1185 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1187 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1189 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1191 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1193 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1195 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1197 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1199 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1201 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1203 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1205 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1207 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1209 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1211 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1213 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1215 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1217 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1219 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1221 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:1227 M:283 W: Missing Blank Line separator, <400> field identifier
L:1241 M:283 W: Missing Blank Line separator, <400> field identifier
L:1255 M:283 W: Missing Blank Line separator, <400> field identifier
L:1269 M:283 W: Missing Blank Line separator, <400> field identifier
L:1283 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/765,120

DATE: 09/01/2004

TIME: 12:45:37

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J765120.raw

L:1297 M:283 W: Missing Blank Line separator, <400> field identifier
L:1311 M:283 W: Missing Blank Line separator, <400> field identifier
L:1325 M:283 W: Missing Blank Line separator, <400> field identifier
L:1339 M:283 W: Missing Blank Line separator, <400> field identifier
L:1353 M:283 W: Missing Blank Line separator, <400> field identifier
L:1367 M:283 W: Missing Blank Line separator, <400> field identifier
L:1381 M:283 W: Missing Blank Line separator, <400> field identifier
L:1395 M:283 W: Missing Blank Line separator, <400> field identifier
L:1409 M:283 W: Missing Blank Line separator, <400> field identifier
L:1419 M:283 W: Missing Blank Line separator, <400> field identifier
L:1429 M:283 W: Missing Blank Line separator, <400> field identifier
L:1439 M:283 W: Missing Blank Line separator, <400> field identifier
L:1449 M:283 W: Missing Blank Line separator, <400> field identifier
L:1450 M:112 C: (48) String data converted to lower case,
L:1451 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:35
L:1451 M:112 C: (48) String data converted to lower case,
L:1451 M:252 E: No. of Seq. differs, <211> LENGTH:Input:83 Found:84 SEQ:35
L:1457 M:283 W: Missing Blank Line separator, <400> field identifier
L:1458 M:112 C: (48) String data converted to lower case,
L:1459 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:36
L:1459 M:112 C: (48) String data converted to lower case,
L:1465 M:283 W: Missing Blank Line separator, <400> field identifier
L:1466 M:112 C: (48) String data converted to lower case,
L:1467 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:37
L:1467 M:112 C: (48) String data converted to lower case,
L:1469 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:37
L:1473 M:283 W: Missing Blank Line separator, <400> field identifier
L:1474 M:112 C: (48) String data converted to lower case,
L:1475 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:84 SEQ:37
L:1475 M:112 C: (48) String data converted to lower case,